

~~1/5~~

1/8

09/284327

## Amino Acid Sequence of EGIII

MKFLQVLPALIPAALAQTSCDQWATFTGNGYTVSNNLWGASAGSGFGCVTAVSLSGGAHADW  
QWSGGQNNVKSQNSQIAIPQKRTVNSISSMPTTASWSYSGSNIRANVAYDLFTAANPNHVT  
YSGDYELMIWLGKYGDIGPIGSSQGTVNVGGSWTLYYGYNGAMQVYSFVAQTNTTNYSGDV  
KNFFNYLRDNKGYNAAAGQYVLSYQFGTEPFTGSGTLNVAWTASIN

FIGURE 1



# FIG. 2

	10	20	30	40	50	60	70
EG3 IN. PRO	NNLWGASAGS-GFGCVTAVSLSG-GA-SWHADWQWSGGQNNVKSYPNS-----QIAIPQ-KRTVNSISS	60					
FUSEQIN. PRO	NNFWGKDSGT-GDQCTHVNNNANGA-GWDVEWNWSGGKDNVKSYPNS-----ALLIGEDKKTISSITN	62					
GLIOIN. PRO	NNKWQGSGS-GSQCLTIDKTWDSNV-AFHADWSWSGGTNNVKSYPKR-----RSEFSRGKK-VSSIGT	61					
ACRHYPO. PRO	---WGPRSAESGEQCTTNNGLSDDGTLSSWSVEWTWVGAPSSVKSYPN-----VFVEAEPRPLSEVSS	59					
ASPKAWA1. PRO	QNLWGEYQGT-GSQCVYVDKLSSSGA-SWHTKWTWSGGEGTVKSYSNS-----GLTF-D-KKLVSQVSS	60					
ASPCAU1. PRO	NNLWGKDAGS-GSQCTTVNSASSAGT-SWSTKWNWSGGENSVKSYANS-----GLTF-N-KKLVSQISQ	60					
HUMIN. PRO	NNLWGKDTATSGWQCTYLDGTNNGGI-QWSTAWEWQAGAPDNVKSYPV-----GKQIORGRK-ISDINS	62					
11AG8IN. PRO	NNRWGTSAT----QC----INVTGNGFEITQADGSVPTNGAPKSYPSVYDGCHYGNC-APRTTLPMRISS	61					
ERWCARIN. PRO	NNVWGKDEI----KG-WQQTIFYNSPISMGWNWHWPSSSTHSVKAYPSLVSGWHWTAGYTENSGLPIQLSS	65					
GLIO314. PRO	NNLWGMGSGS-GSQCTYVDKVWAEGV-AWHTDWSWSGGDNNVKSYPYS-----GRELGTKRI-VSSIKS	61					
GLIO3HYP. PRO	NNLWGQDNG-SGSQCLTVEGVTDGLA-AWSSTWWSWSGGSSSVKSYSNA-----VLSAEAA--ISAISS	60					
HGRIS. PRO	NNLWGKDTATSGWQCTYLDGTNNGGI-QWSTAWEWQAGAPDNVKSYPV-----GKQIORGRK-ISDINS	62					
RHMARIN. PRO	NNVWGAETA----QC----IEVGLTENGFTITRADH--DNGNNVAAYPATYFGCHWAPAIRAIRDCAARAGAV	62					
SLIVIN. PRO	NNRWGSTAP----QC----VTATDTGFRVTQADGSAPTNGAPKSYPSVFNGCHYTNC-SPGTDLPVRLDT	61					
PENNOT. PRO	---WGKDSGS-GSQCASVNSISDSGV-SWSTTWNWSGGEDNVKSYPNS-----GLVALK-KQPVSDISS	58					
PHANHYP. PRO	---WGKDSG-TGSQCLTVDGISSGLL-KWSATWSWSGGPYNVKSYPNA-----VLQAPAA--ASAISS	57					
F42HYPO. PRO	-----S-----QCTTFESLSGNTI-VWNTKWSWSGGQGVKSFANA-----ALQFTPK--LSSVKS	49					
EMDESHP. PRO	NNLWGXDADSGSQCTGVDSANGNSI-SWHTTWSWSGGSSSVKSYANA-----AYQFTSTK--LNSLSS	61					
MYCINS. PRO	-----	1					
CHBRAS. PRO	NNFWGQSRATSGSQCTYLDSSSNSGI-HWHTTWTWEGGEVKSAYAS-----GROVSTGLT-IASIDS	62					

	IPSSASW	-YSGTDIRA	-NVAYDL	-FTAADPNHATSSGDYELMIW		
	80	90	100	110		
EG3IN.PRO	MPTTASWS	-YSGSNIRA	-NVAYDL	-FTAANPNHVITYSGDYELMIW	102	
FUSEQIN.PRO	MQSTAEWK	-YSGDNLRA	-DVAYDL	-FTAADPNHETSSSGEYELMIW	104	
GLIOIN.PRO	INGGADWD	-YSGSNIRA	-NVAYGI	-FTSADPNHVTSSGDYELMIW	103	
ACRHYPO.PRO	IQAEWAWITYSGAGDFTT	-NVAFDI	-FTGETAD		89	
ASPKAWA1.PRO	IPTSVTWS	-QDDTNVQA	-DVSVDL	-FTAANADHATSSGDYELMIW	102	
ASPACU1.PRO	IPTTARWS	-YDNTGIRA	-DVAYDL	-FTAADINHVTWSGDYELMIW	102	
HUMIN.PRO	MRTSVSWT	-YDRTDIRA	-NVAYDV	-FTARDPDHPNWGGDYELMIW	104	
11AG8IN.PRO	IGSAPSSVSRYRTGNGVYNAAYDIWLDPTPRTNGVNR	--TEIMI			104	
ERWCARIN.PRO	NKSITSNVITYSIKATGTYNAAAYDIWFHTTDKANWDDSSPTDELMIW				110	
GLIO314.PRO	ISSGADWD	-YTGSNLRA	-NAAAYDI	-FTSANPNHATSSGDYELMIW	103	
GLIO3HYP.PRO	IPSKWEWRSYTGTDIVA	-NVAYDL	-FSNTDCGDT	---EYELMIW	100	
HGRIS.PRO	MRTSVSWT	-YDRTDIRA	-NVAYDV	-FTARDPDHPNWGGDYEFMIW	104	
RHMARIN.PRO	RRARELDVT	-PI	-TTGRWNAAYDIWFSPVTNSGNGYSGGAEIMI		105	
SLIVIN.PRO	VSAAPKSSISYGFVDGAVYNASYDIWLDPTARTDGVNQ	--TEIMI			104	
PENNOT.PRO	IPSSVKNW	-YDNTDIRA	-DVAYDL	-FTAADINHDTSSGDYE	96	
PHANHYPO.PRO	IPSKWQWESYTGSNVIA	-NVAYDL	-FSNSDCG		87	
F42HYPO.PRO	IDSTWKWKSYSGSNIVA	-DVAYDM	-FLSTSPGGDH	---NY	84	
EMDESHYP.PRO	IPTSWKWQ	-YSTTDIVA	-NVAYDL	-FTSSSAGGDS	---EYEFMIW	100
MYCINS.PRO	-----	-A	-NVAYDL	-FTAADPNHATSSGDYELMIW	27	
CHBRAS.PRO	MOTSVSWE	-YNTTDIOA	-NVAYDI	-FTAEDPDHEHSSGDYELMIW	104	

**FIGURE 3**

Percent Divergence

Percent Similarity

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
1		51.0	52.9	27.0	49.0	56.9	43.1	17.6	18.6	55.9	37.0	42.2	16.7	14.7	50.0	39.1	36.9	36.0	88.9	46.1	1
2	43.1		48.5	22.5	47.1	55.9	43.3	15.4	21.2	54.4	37.0	41.3	15.4	13.5	55.2	40.2	34.5	34.0	88.9	42.3	2
3	42.6	48.5		21.3	42.2	49.0	41.7	15.5	22.3	68.9	38.0	41.7	16.5	12.6	50.0	40.2	34.5	33.0	85.2	44.7	3
4	66.7	66.3	70.6		25.8	31.5	31.5	18.0	20.2	22.5	34.8	31.5	12.4	16.9	28.1	33.3	28.6	33.7	22.2	29.2	4
5	44.6	51.0	53.5	63.1		65.7	40.2	12.7	22.5	51.0	38.0	39.2	11.8	12.7	59.4	41.4	36.9	40.0	81.5	49.0	5
6	36.6	41.2	46.5	61.9	34.3		46.1	16.7	24.5	52.0	46.0	44.1	13.7	15.7	69.8	44.8	41.7	47.0	85.2	47.1	6
7	54.5	50.5	56.3	60.5	52.5	48.5		21.2	19.2	45.6	34.0	98.1	19.2	14.4	49.0	35.6	28.6	41.0	74.1	61.5	7
8	75.0	77.7	76.3	80.0	77.2	72.8	71.0		24.0	19.4	21.0	21.2	24.0	66.3	14.6	16.1	14.3	20.0	22.2	18.3	8
9	73.5	71.0	73.7	78.6	77.6	71.4	73.7	68.3		22.3	19.0	17.3	23.8	21.2	20.8	16.1	16.7	20.0	37.0	22.1	9
10	42.6	43.7	31.1	68.2	46.5	45.5	52.4	72.0	72.7		40.0	44.7	17.5	14.6	55.2	41.4	34.5	37.0	85.2	49.5	10
11	55.2	53.1	55.1	58.8	55.2	47.9	54.5	70.3	71.9	53.1		34.0	16.0	16.0	41.7	72.4	45.2	50.0	44.4	33.0	11
12	55.4	52.4	56.3	60.5	53.5	50.5	1.9	71.0	75.8	53.4	54.5		18.3	14.4	47.9	34.5	28.6	42.0	70.4	61.5	12
13	73.1	75.8	74.5	79.7	80.6	77.4	72.3	67.0	69.5	72.3	76.9	73.4		21.2	11.5	12.6	10.7	14.0	33.3	15.4	13
14	80.4	81.9	76.3	81.2	81.5	80.4	74.2	33.7	73.1	77.4	76.9	74.2	72.0		13.5	13.8	14.3	15.0	22.2	15.4	14
15	46.3	41.7	48.4	60.0	37.9	27.4	48.4	76.7	73.9	45.3	47.8	49.5	81.6	84.9		47.1	35.7	40.6	74.1	50.0	15
16	54.2	54.1	54.1	61.2	55.4	50.6	57.0	74.7	74.7	51.8	27.6	58.1	79.5	83.5	44.0		44.0	41.4	33.3	31.0	16
17	55.6	56.6	61.4	67.5	59.3	55.6	68.7	80.8	81.9	59.0	56.0	68.7	87.2	83.3	58.5	54.4		56.0	25.9	35.7	17
18	51.0	56.1	58.2	59.5	51.0	45.8	53.5	75.3	69.1	56.1	42.9	52.5	77.5	78.7	48.9	51.8	40.2		44.4	46.0	18
19	11.1	11.1	14.8	57.1	18.5	14.8	25.9	68.0	51.9	14.8	37.5	29.6	55.6	72.0	13.0	35.7	57.9	41.7		81.5	19
20	50.5	52.4	53.4	61.6	45.5	49.5	38.5	71.0	73.7	48.5	57.6	38.5	75.5	74.2	48.4	62.8	61.4	48.5	18.5		20
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	

EG3IN.PRO  
FUSEQIN.PRO  
GLION.PRO  
ACRHYPO.PRO  
ASPKAWA1.PRO  
ASPACU1.PRO  
HUMIN.PRO  
11AG8IN.PRO  
ERWCARIN.PRO  
GLIO314.PRO  
GLIO3HYP.PRO  
HGRIS.PRO  
RHMARIN.PRO  
SLVIN.PRO  
PENNOT.PRO  
PHANHYPO.PRO  
F42HYPO.PRO  
EMDESHYP.PRO  
MYCINS.PRO  
CHBRAS.PRO

FIGURE 4

09/284327

09/284327

5/12

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
1		51.0	52.9	27.0	49.0	56.9	43.1	17.6	18.6	55.9	37.0	42.2	16.7	14.7	50.0	39.1	36.9	36.0	88.9	46.1	1
2	43.1		48.5	22.5	47.1	55.9	43.3	15.4	21.2	54.4	37.0	41.3	15.4	13.5	55.2	40.2	34.5	34.0	88.9	42.3	2
3	42.6	48.5		21.3	42.2	49.0	41.7	15.5	22.3	68.9	38.0	41.7	16.5	12.6	50.0	40.2	34.5	33.0	85.2	44.7	3
4	66.7	66.3	70.6		25.8	31.5	31.5	18.0	20.2	22.5	34.8	31.5	12.4	16.9	28.1	33.3	28.6	33.7	22.2	29.2	4
5	44.6	51.0	53.5	63.1		65.7	40.2	12.7	22.5	51.0	38.0	39.2	11.8	12.7	59.4	41.4	36.9	40.0	81.5	49.0	5
6	36.6	41.2	46.5	61.9	34.3		46.1	16.7	24.5	52.0	46.0	44.1	13.7	15.7	69.8	44.8	41.7	47.0	85.2	47.1	6
7	54.5	50.5	56.3	60.5	52.5	48.5		21.2	19.2	45.6	34.0	98.1	19.2	14.4	49.0	35.6	28.6	41.0	74.1	61.5	7
8	75.0	77.7	76.3	80.0	77.2	72.8	71.0		24.0	19.4	21.0	21.2	24.0	66.3	14.6	16.1	14.3	20.0	22.2	18.3	8
9	73.5	71.0	73.7	78.6	77.6	71.4	73.7	68.3		22.3	19.0	17.3	23.8	21.2	20.8	16.1	16.7	20.0	37.0	22.1	9
10	42.6	43.7	31.1	68.2	46.5	45.5	52.4	72.0	72.7		40.0	44.7	17.5	14.6	55.2	41.4	34.5	37.0	85.2	49.5	10
11	55.2	53.1	55.1	58.8	55.2	47.9	54.5	70.3	71.9	53.1		34.0	16.0	16.0	41.7	72.4	45.2	50.0	44.4	33.0	11
12	55.4	52.4	56.3	60.5	53.5	50.5	1.9	71.0	75.8	53.4	54.5		18.3	14.4	47.9	34.5	28.6	42.0	70.4	61.5	12
13	73.1	75.8	74.5	79.7	80.6	77.4	72.3	67.0	69.5	72.3	76.9	73.4		21.2	11.5	12.6	10.7	14.0	33.3	15.4	13
14	80.4	81.9	76.3	81.2	81.5	80.4	74.2	33.7	73.1	77.4	76.9	74.2	72.0		13.5	13.8	14.3	15.0	22.2	15.4	14
15	46.3	41.7	48.4	60.0	37.9	27.4	48.4	76.7	73.9	45.3	47.8	49.5	81.6	84.9		47.1	35.7	40.6	74.1	50.0	15
16	54.2	54.1	54.1	61.2	55.4	50.6	57.0	74.7	74.7	51.8	27.6	58.1	79.5	83.5	44.0		44.0	41.4	33.3	31.0	16
17	55.6	56.6	61.4	67.5	59.3	55.6	68.7	80.8	81.9	59.0	56.0	68.7	87.2	83.3	58.5	54.4		56.0	25.9	35.7	17
18	51.0	56.1	58.2	59.5	51.0	45.8	53.5	75.3	69.1	56.1	42.9	52.5	77.5	78.7	48.9	51.8	40.2		44.4	46.0	18
19	11.1	11.1	14.8	57.1	18.5	14.8	25.9	68.0	51.9	14.8	37.5	29.6	55.6	72.0	13.0	35.7	57.9	41.7		81.5	19
20	50.5	52.4	53.4	61.6	45.5	49.5	38.5	71.0	73.7	48.5	57.6	38.5	75.5	74.2	48.4	62.8	61.4	48.5	18.5		20
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	

EG3IN.PRO  
FUSEQIN.PRO  
GLIOIN.PRO  
ACRHYPO.PRO  
ASPKAWA1.PRO  
ASPACU1.PRO  
HUMIN.PRO  
11AG8IN.PRO  
ERWCARIN.PRO  
GLIO314.PRO  
GLIO3HYP.PRO  
HGRIS.PRO  
RHMARIN.PRO  
SLVIN.PRO  
PENNOT.PRO  
PHANHYPO.PRO  
F42HYPO.PRO  
EMDESHYP.PRO  
MYCINS.PRO  
CHBRAS.PRO

PERCENT DIVERGENCE

PERCENT SIMILARITY

FIG..4

6/8

PCT/US 98/26552

09/284327

## FIGURE 6

	1		60
T. reesei	M.....	KF.LQVLPALIPAALQAQS.....	CDQWATFTGNG..YTV
H. schweinitzii	M.....	KF.LQVLPAILPAALQAQS.....	CDQYATFSGNG..YIV
A. aculeatus	M.....	KAFHL.LAALAGAAVAQQAQ.....	LCDQYATYTGTV..YTI
A. kawachii	M.....	KLST.LSLFAATAMGQT.....	MCSQYDSASSPP..YSV
A. kawachii_2	M.....	KAFHL.LAALSGAAVAQQAQ.....	LCDQYATYTGTV..YTI
A. oryzae	M.....	KLST.LATLVATAFSQE.....	LCAQYDSASSPP..YSV
H. grisei	M.....	LKSALLGAAAVSVQASIPTIPANLEPRQIR..	SLCELYGYWSGNG..YEL
H. insolens	M.....	LKSALLGPAAVSVQASIPTIPANLEPRQIR..	SLCELYGYWSGNG..YEL
Chaetomium brasiliense	M.....	KLTLVLFVSSLA.....	AATPLGWRERQQQVSLCGQSSSSWSGNG..YQL
F. equseti	M.....	KSTLLAGAFAPLAFKD.....	LCEQYGYLSSDG..YSL
F. javanicum_1	M.....	KSAIVA.ALAGLAAASPTRLIPRGQ.....	FCGQWDSETAGA..YTI
F. javanicum_2	M.....	K.FFGVVSASLAATAVATPTPTETIEKRDTTWCDAFGSLATSG..	YTV
G. roseum_1	M.....	KANIVILSLFAPLAQAQ.....	LCCQYSSNTQGG..YIF
G. roseum_2	M.....	KSIIFFGLATLVAAAPSONPRTQPLEKRATTLCGQWDSVETGG..	YTI
G. roseum_3	M.....	KFQLLSLTAFAPLSLAA.....	LCCQYQSQSQGG..YIF
G. roseum_4	M.....	KTGIAYLAAVLPLA.MAES.....	LCDQYAVLSRDG..YNF
Memnoniella echinata	M.....	KVAAL.LVALSPLAF.AQS.....	LCDQYSYSSNG..YEF
Emericella desertoru	M.....	K.LLALSLSVLSAASAASIL.SNTFTTRSD..	FCGQWDTATVGN..FIV
Actinomyces_11AG8	MRS.....	HPRS..ATM.TVLVVLASLGALLTAAAPAQAQNCIDRYGTTIQD..	RYVV
S. lividans_CelB	MRTLRPQARAPRGLAALGAVLAALFVSSLVTAAPQAQADTTICEPFGTTTIQ..	RYVV	
Rhodothermus marinus	MNVMR..	AVLVLSLLLFGCDWL.FPDGNGKEPEPEPEPTVELCGRWDARDVAGGRYRV	
Erwinia carot	MQTVNTQPHRIFRVLPAVFSLLLSSSLTVSAASSNDADKLYF.....	GNNKYLL	
	61		120
T. reesei	SNNLWGASAGSGF..	GC.V.TAVSLSGG.ASWHADWQWSGGQNNVKSQNS.....	
H. schweinitzii	SNNLWGASAGSGF..	GC.V.TSVSLNGA.ASWHADWQWSGGQNNVKSQNV.....	
A. aculeatus	NNNLWGKDAGSG..	SQCTTVNSASSAG.TSWSTKWNWSGGGNSVKSYSANS.....	
A. kawachii	NQNLWGEYQGTG..	SQCVYVDKLSGG.ASWHTKWTWSGGEGTVKSYSNS.....	
A. kawachii_2	NNNLWGKDAGSG..	SQCTTVNSASSAG.TSWSTKWNWSGGGNSVKSYSANS.....	
A. oryzae	NNNLWQDSDGTGFTSQCVYVDNLSGG..	AAWHTTWTWNGGEGSVKSYSNS.....	
H. grisei	LNNLWGKDTATS..	GWCTYLDGTNNGG.IQWNTAWEWQCAPDNVKSYPV.....	
H. insolens	LNNLWGKDTATS..	GWCTYLDGTNNGG.IQWNTAWEWQCAPDNVKSYPV.....	
Chaetomium brasiliense	NNNLWQSRATS..	GSQCTYLDSSNSG.IHWHTTWTWEGGEGSVKSYSANS.....	
F. equseti	NNNVWGKDSGTG..	QCTHVNWNANG.AGWDVEWNNWSGGKDNVKSYPNS.....	
F. javanicum_1	YNNLWGKDNES..	GEQCTTNSGEQSDGSIASVIEWSWTGGQGVKSYPNA.....	
F. javanicum_2	YHNNWGKGDATS..	GSQCTTFTSVSNNSFV.WSTSWTWAGGAGKVSYSNV.....	
G. roseum_1	NNNMWGMGSGSGS..	QCTYVDKVAEG.VAWHTDWSWGGDNVKSYPNS.....	
G. roseum_2	YNNLWQDNG..	S.GSQCLTVEGV.TDGLAASSTWSWGGSSSVKSYSNA.....	
G. roseum_3	NNNKWQGGSGSGS..	QCLTIDKTWDSN.VAFHADWSWGGTNNVKSYPNA.....	
G. roseum_4	NNNWEAATGTG..	QCTYVDSTSSG.VSWHSDWTWSGSEIKSYPNS.....	
Memnoniella echinata	NNNMWGRNSGQCN..	QCTYVDYSSPNC.VGWRVNNWSGGDNVKSYPNS.....	
Emericella desertoru	YNNLWQDNDAS..	GSQ.TGVDSANGNISWHTTWSWGGSSSVKSYSNA.....	
Actinomyces_11AG8	QNNRWGTSAT....	QCINVT..GNGFEITQADGS..VPTNGAPKSYPSVYDGCHYG...	
S. lividans_CelB	QNNRWGSTAP....	QCVTAT..DTGFRVTQADGS..APTNGAPKSYPSVFNCHYT...	
Rhodothermus marinus	INNVAWGAETA....	QCIEVGLTGNFTITRADHD..NGNNVA..AYPAIFYGCHWAPAR	
Erwinia carot	FNNVWGKDEIKGWQQTIFYNSPISMG....	WN..WHWPSSTHSVKAYPSLVSGWHWTAG..	
	121		180
T. reesei	.QIAIP.QKRTVNSISSMPTTASW..	SYSGSNIRANVAYDL.FTAANPNHVTYSGDYEL	
H. schweinitzii	.QINIP.QKRTVNSIGSMPTTASW..	SYSGSDIRANVAYDL.FTAANPNHVTYSGDYEL	
A. aculeatus	.GLTF..NKKLVQSISQIPTARW..	S.YDNTGIRADVAYDL.FTAADINHVTWSGDYEL	
A. kawachii	.GLTF..DKKLVSQVSSIPTVW..	SQD..DTNVQADVSVDL.FTAADINHVTWSGDYEL	
A. kawachii_2	.GLSF..NKKLVQSISHIPTAARW..	S.YDNTCIRRGAYDL.FTAADINHVTWSGDYEL	
A. oryzae	.AVTF..DKKLVSQVSIPTDVEW..	SQDFTNTNVNADVAYDL.FTAADQNHVTYSGDYEL	
H. grisei	.GKQIQGRK..ISDINSMTSVSW..	TYDRTDLRANVAYDV.FTARDPDHPNWGGDYEL	
H. insolens	.GKQIQGRK..ISDINSMTSVSW..	TYDRTDLRANVAYDV.FTARDPDHPNWGGDYEL	
Chaetomium brasiliense	.GRQVSTGLT..IASIDSMQTSVSW..	EYNTTDIQANVAYDI.FTADPDHEHSSGDYEL	
F. equseti	.ALLIGEDKKTISSITNMQSTAEW..	KYSGDNLRADVAYDL.FTADPNHETSSGEYEL	
F. javanicum_1	.VVEI..EKKTLGEVSSIPSA..	W.DWYTGNGIIVANVAYDL.FTSSTESGDA..EYEF	
F. javanicum_2	.ALEK..INKKISDIKSVSTR..	W.IWRYTGTKMIANVAYDL.WFAPTASSNN..AYEI	
G. roseum_1	.GRELGT..KRIVSSIKSISGADW..	DYTGSLNRANAAYDI.FTSANPNHATSSGDYEV	
G. roseum_2	.VLSA..EAARISAISIPSK..	W.EWSTGTDIVANVAYDL.FSNTDCGDTT..EYEI	
G. roseum_3	.GLEFSR..GKKVSSIGTINGGADW..	DYSGSNIRANVAYGI.FTSADPNHVTSSGDYEL	
G. roseum_4	.GLDLPE..KKIVTSIGSISTGAEW..	SYSGSDIRADVAYDT.FTADPNHATSSGDYEV	
Memnoniella echinata	.GRQLPT..KRIVSWIGSLPTTVSW..	NYQGNLNRANVAYDL.FTAANPNHNPSSGDYEL	
Emericella desertoru	.AYQF..TSTKLNSLSIPTS..	W.KWQYSTTDIVANVAYDL.FTSSSAGGDS..EYEI	
Actinomyces_11AG8	...NCAPRTTLMRISISGSAPSSSVRYRTGNGVY..	NAAYDIWLDPTPTNGVNR..TEI	
S. lividans_CelB	...NCSPGTDLPVRLDTVSAAPSSISYGFVDGAVY..	NASYDIWLDPTARTDGVNQ..TEI	
Rhodothermus marinus	AIRDCARAGAVRRRAHLDVTP.....	ITTGRW.NAAYDIWFSPTVNSGNGYSGGAE	
Erwinia carot	...YTENSGPLIQLSSNKSITSNTVTSIKATGTY..	NAAYDIWFHTTDKANWDSSPTDEL	
	181		240
T. reesei	MIWLKGYGDIGPIGSS....	QGTVNVGGQSWTLYYGYNGAMQV.....	YSFVAQT.NTT
H. schweinitzii	MIWLKGYGDIGPIGSS....	QGTVNVGGQSWTLYYGYNGAMQV.....	YSFVAQS.NTT
A. aculeatus	MIWLARYGGVQPIGSG....	IATATVDGQTWELWYG.....	ANGSKQTSYFVAPT.PIT
A. kawachii	MIWLARYGSVQPIGKQ....	IATATVGGKSEWV..YGTSTQAGAEQKTSYFVAGS.PIN	
A. kawachii_2	MIWLARYGGVQPLGSG....	IATATVEGQTWELWYG.....	VNGAQKTSYFVAAN.PIT

09/24/27

```

MIWLARYGTIQPIGTQ...IDTATVEGHTWELWVGMMNGSMKV...GTTIQAGAEQKTSYFSVAT.PIN
MIWLARYGGIYPIGTF...HSQVNLAGRTWDLWVGMMNRV.....YSFLPPSGDIR
MIWLARYGGIYPIGTF...HSQVNLAGRTWDLWVGMMNRV.....YSFLPPSGDIR
MIWLARYNVSPIGSS...VATATVGGDTWDLFAGANGMEV.....YSFVAENT.MN
MVWLARIGGVQPIGSL...QTSVTIEGHTWELWVGMMNGSMKV.....FSFVAPT.PVN
MIWLSALGGAGPISNDGSP...ATAELAGTSPKWLQCKGNQMVT.....FSFVAESDV.N
MIWLSAGGALPISTPGKGVIDRPTLAGIPWDVYKPGNGDVTV.....ISFVAESNQ.G
MIWLANLGGLTPIGSP...IGTVKAAGRWDWELWDGYNGAMRV.....YSFVAPS.QLN
MIWLSALGGAGPISSTGSS...IATVTIAGASWNFLQCGNQNMV.....FSFVAESDQ.K
MIWLGKGLDIYPIGNS...IGRVEAANREWDLFVGGYNGAMKV.....FSFVAPS.PVT
MIWLANLGGLTPIGSP...IGTVKAAGRWDWELWDGYNGAMRV.....YSFVAPS.QLN
MIWLGRLGNVPYIGNQ...IATVNIAQGWNNLLYGYNGAMQV.....YSFVSPN.QLN
MIWLAALGGAGPISSTGSS...IATVTLGGVTWSLYSGPNCSMQV.....YSFVASSTT.E
MIWFNRVGPVQPIGSP...VGTAHVGGRSWEVWTSNGNSNDVI.....SFLAPSA.IS
MIWFNRVGPPIQPIGSP...VGTAHVGGRTWEVWSSGGNGSNDVL...SFVAPSA.IS
MIWLNWNGVMPGGSR...VATVELAGATWEVWAGDWDWNWNYA...YRRTTPT.TS
MIWLNDTNA.....GPAGDYIETVFLGDSSWNVPFKGWINADN.GGGWNVPFSVHTSGTN

```

```

241
NYSGDVKNFFNYLRDNKGYNAGQYV..LSYQFGTEPF..TGSCT.LNVASWTASI.N..
SYSGDVKNFFNYLRDNKGYNAGQYV..LSYQFGTEPF..TGSCT.LNVASWTASI.N..
SFQGDVNDFFKYLTONHGFPASSQYLI..TLQFGTEPF..TGGPATLSVNWSASVQQA..
SWSGDIKDFFNLYLTONHGFPASSQHLI..TLQCGTEPF..TGGPATFTVDNWTASVN..
SFQGDINDFFKYLTONHGFPASSQYLILALQFGTEPF..TGGPATLNVDWSASVQ..
TFGGDIKKFFDYITSKHSFPASAQYLI..NMQGFTEPFPTTGGPVFTVPNWTSASVN..
DFSCDIKDFFNLYLERNHGYAPAREQNLIV..YQVGTECF..TGGPARFTCRDFRADL..
DFSCDIKDFFNLYLERNHGYAPAREQNLIV..YQVGTECF..TGGPARFTCRDFRADL..
SFSGDVKDFFDYLEQNVGFPVDDQYLLV..FLGSEAF..TGGPATLSVSQFSANI..
NFNADIKQFWDYLTKSQNFADNQYL..LTFQFGTEPF..TGDNAKFTVTNFAHLK..
NFCGDLADFTDYLVNDHNGVSSSQ..ILQSVGAGTEPF..EGTNVAFPTNNYHADVE..
NFQADLKEFLNYLTSKQGLPSNY..VATFSQAGTEPF..EGTNVAVLTSAYTISVN..
SFDGEIMDFFVYVVKDMRGFPADSQHL..LTVQFGTEPI..SGSGAKFSVSHWSAKLG..
SFSGDLNDDFYQYVLVDSQYSGSQ..CLYSIGAGTEPF..TGTDAEFTITGYSVSVSAGD..
LFDGNIMDFFYVYVMDMGQYVMDKQYL..LSLQFGTEPF..TGSNANFSCWYFGAKI..
SFDGEIMDFFVYVVKDMRGFPADSQHL..LTVQFGTEPI..SGSGAKFSVSHWSAKLG..
YFSGNVKKDFFTYLYQYNRAYPADSQYL..ITYQFGTEPF..TQGNVAFTVSNWSAQQNN..
SFSADLMDFFNLYLAENQGLSSSQ..YLTHVQAGTEPF..TGTDAFTLVSSYSVSVS..
SWSFVDVKDFVD.QAVSHGLATPDWYLT..SIQAGFEWP..EGGTGLAVNFSFSSAVNAG..
GWSFDVMDVFR.ATVARGLAENDWYLT..SVQAGFEWP..QNGAGLAVNFSNSTVETGT..
VSELDLKAFD.DAVARGYIRPEWYLT..AVETGFELW..EGGAGLRTADFSVTVQ..
A.SLNIRHFTDYLVQTKQWMSDEKYIS..SVEFGTEIF..GGDGQIDITEWRVDVK..

```

```

301                                     360
.....
F.....EPWQNGAGLAVNSF.....
.....
.....W.....
.....W.....
.....A.....
.....
.....
SGCDETTTSSQAQSSTVETSTATQPQS...SSTVVPTVTLS.QPSNESTTTPVQSQ....
.....
.....
..GGNGGTPGTPAACQVSYSTHTWPGGFTVDTTITNTGSTPVDGWELDFTLPAGHVTSTA
PGGTDPGDPGGPSACA VSYGTNVWQDGFTADVTVTNTGTAPVDGWQLAFTLP SGQRITNA
.....

```

[illegible]

Fig 6 (continued)

WNALIS PASGAVTARSTGSNGRIAANGGTQSFGFQGTSSGTGFNAPAGGRLNGTSCTVR  
WNASLTPSSGSVTATGASHNARIAP.GGSLSFGFQGTYGGA.FAeptGfRLNGTACTTV

09/284327

[illegible]

Fig 6 (Continued)